

SEQUENCE LISTING

<110> KAO CORPORATION

<120> Mutant Bacillus

<130> KS0816

<150> JP 2004-062852

<151> 2004.03.05

<160> 28

<170> PatentIn Ver. 3.1

<210> 1

<211> 371

<212> PRT

<213> Bacillus subtilis

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35 40 45

Met Asp Glu Tyr Tyr Glu Phe Leu Gly Glu Gln Gly Val Glu Leu Ile
50 55 60

Ser Glu Asn Glu Glu Thr Glu Asp Pro Asn Ile Gln Gln Leu Ala Lys
65 70 75 80

Ala Glu Glu Glu Phe Asp Leu Asn Asp Leu Ser Val Pro Pro Gly Val
85 90 95

Lys Ile Asn Asp Pro Val Arg Met Tyr Leu Lys Glu Ile Gly Arg Val
100 105 110

Asn Leu Leu Ser Ala Lys Glu Glu Ile Ala Tyr Ala Gln Lys Ile Glu
115 120 125

Glu Gly Asp Glu Glu Ser Lys Arg Arg Leu Ala Glu Ala Asn Leu Arg
130 135 140

Leu Val Val Ser Ile Ala Lys Arg Tyr Val Gly Arg Gly Met Leu Phe
145 150 155 160

Leu Asp Leu Ile His Glu Gly Asn Met Gly Leu Met Lys Ala Val Glu
165 170 175

Lys Phe Asp Tyr Arg Lys Gly Tyr Lys Phe Ser Thr Tyr Ala Thr Trp
180 185 190

Trp Ile Arg Gln Ala Ile Thr Arg Ala Ile Ala Asp Gln Ala Arg Thr
195 200 205

Ile Arg Ile Pro Val His Met Val Glu Thr Ile Asn Lys Leu Ile Arg
210 215 220

Val Gln Arg Gln Leu Leu Gln Asp Leu Gly Arg Glu Pro Thr Pro Glu
225 230 235 240

Glu Ile Ala Glu Asp Met Asp Leu Thr Pro Glu Lys Val Arg Glu Ile
245 250 255

Leu Lys Ile Ala Gln Glu Pro Val Ser Leu Glu Thr Pro Ile Gly Glu
260 265 270

Glu Asp Asp Ser His Leu Gly Asp Phe Ile Glu Asp Gln Glu Ala Thr
275 280 285

Ser Pro Ser Asp His Ala Ala Tyr Glu Leu Leu Lys Glu Gln Leu Glu
290 295 300

Asp Val Leu Asp Thr Leu Thr Asp Arg Glu Glu Asn Val Leu Arg Leu
305 310 315 320

Arg Phe Gly Leu Asp Asp Gly Arg Thr Arg Thr Leu Glu Glu Val Gly
325 330 335

Lys Val Phe Gly Val Thr Arg Glu Arg Ile Arg Gln Ile Glu Ala Lys
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Ala Leu Arg Lys Leu Arg His Pro Ser Arg Ser Lys Arg Leu Lys Asp
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Phe Leu Glu
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<213> *Bacillus subtilis*

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aacggatgcg tccgcgcgtg aggatttccg taatatggac ggcaatatgc ctttggctct 300
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acagaccaac catagagttg aagtaatitt tacaaaagaa aatgagacgg ctgtatgagcg 720

gatagaaaag ctcgctcagg ctttgaataa tattgcact caaattcacg ttgcgacac	780
tgactatact gagcagtggg cgatttcgg acagggggca ttgcggaaat cggcccgaaa	840
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gtggaggcgg ggagacttag attaagtta cgctttttg cccaaatactg tataatattt	1020
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caaaatcaaa atgagtgata aggtccgtac aagcgagcat gcccgtcaa tggcggctc	180
acagatattc cttgagcccg gcgaagaaat gactgtcaaa gaaatgctga aaggcatcgc	240
aatcgcttcg ggaaatgacg cttccgtcgc catggctgaa tttatccg gctctgaaga	300
agaatttgc aagaaaatga ataaaaaagc aaaagagctg ggattggaaaa atacatccctt	360
taaaaaccca acaggactga ccgaggaagg acactacagc tctgctttagt acatggcaat	420
catggctaag gaattttaga aatacgaatc aattacgaag tttaccggca cgtatgaaga	480
ttatctgcgt gaaaatacag ataaaaagtt ttggcttgc aatacaaatc gccttatcaa	540
attttatccct ggtgttagacg gcgtaaaaac aggctataca ggcgaagcga aatattgtct	600
gactgcttcg gctaaaaaag gaaacatgcg ggccatagcg gttgtattcg gagcgagcac	660
gcctaaagaa agaaacgcgc aagtacaaa aatgcttgc ttcgccttta gccaatatga	720
aacgcattct ttatataaac gaaatcaaac agtagcaaaa gtaaaggta aaaaaggaa	780
acaaaaattt atcgaactca ctacatctga gccgatttca atattgacga aaaaaggcga	840
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<213> *Bacillus* sp. KSM-S237

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Val Asp Gly Gln Met Thr Leu Val Asp Gln His Gly Glu Lys Ile Gln
35 40 45

Leu Arg Gly Met Ser Thr His Gly Leu Gln Trp Phe Pro Glu Ile Leu
50 55 60

Asn Asp Asn Ala Tyr Lys Ala Leu Ser Asn Asp Trp Asp Ser Asn Met
65 70 75 80

Ile Arg Leu Ala Met Tyr Val Gly Glu Asn Gly Tyr Ala Thr Asn Pro
85 90 95

Glu Leu Ile Lys Gln Arg Val Ile Asp Gly Ile Glu Leu Ala Ile Glu
100 105 110

Asn Asp Met Tyr Val Ile Val Asp Trp His Val His Ala Pro Gly Asp
115 120 125

Pro Arg Asp Pro Val Tyr Ala Gly Ala Lys Asp Phe Phe Arg Glu Ile
130 135 140

Ala Ala Leu Tyr Pro Asn Asn Pro His Ile Ile Tyr Glu Leu Ala Asn
145 150 155 160

Glu Pro Ser Ser Asn Asn Asn Gly Gly Ala Gly Ile Pro Asn Asn Glu
165 170 175

Glu Gly Trp Lys Ala Val Lys Glu Tyr Ala Asp Pro Ile Val Glu Met
180 185 190

Leu Arg Lys Ser Gly Asn Ala Asp Asp Asn Ile Ile Ile Val Gly Ser
195 200 205

Pro Asn Trp Ser Gln Arg Pro Asp Leu Ala Ala Asp Asn Pro Ile Asp
210 215 220

Asp His His Thr Met Tyr Thr Val His Phe Tyr Thr Gly Ser His Ala
225 230 235 240

Ala Ser Thr Glu Ser Tyr Pro Ser Glu Thr Pro Asn Ser Glu Arg Gly
245 250 255

Asn Val Met Ser Asn Thr Arg Tyr Ala Leu Glu Asn Gly Val Ala Val
260 265 270

Phe Ala Thr Glu Trp Gly Thr Ser Gln Ala Ser Gly Asp Gly Gly Pro
275 280 285

Tyr Phe Asp Glu Ala Asp Val Trp Ile Glu Phe Leu Asn Glu Asn Asn
290 295 300

Ile Ser Trp Ala Asn Trp Ser Leu Thr Asn Lys Asn Glu Val Ser Gly
305 310 315 320

Ala Phe Thr Pro Phe Glu Leu Gly Lys Ser Asn Ala Thr Asn Leu Asp
325 330 335

Pro Gly Pro Asp His Val Trp Ala Pro Glu Glu Leu Ser Leu Ser Gly
340 345 350

Glu Tyr Val Arg Ala Arg Ile Lys Gly Val Asn Tyr Glu Pro Ile Asp
355 360 365

Arg Thr Lys Tyr Thr Lys Val Leu Trp Asp Phe Asn Asp Gly Thr Lys
370 375 380

Gln Gly Phe Gly Val Asn Ser Asp Ser Pro Asn Lys Glu Leu Ile Ala
385 390 395 400

Val Asp Asn Glu Asn Asn Thr Leu Lys Val Ser Gly Leu Asp Val Ser
405 410 415

Asn Asp Val Ser Asp Gly Asn Phe Trp Ala Asn Ala Arg Leu Ser Ala
420 425 430

Asn Gly Trp Gly Lys Ser Val Asp Ile Leu Gly Ala Glu Lys Leu Thr
435 440 445

Met Asp Val Ile Val Asp Glu Pro Thr Thr Val Ala Ile Ala Ala Ile
450 455 460

Pro Gln Ser Ser Lys Ser Gly Trp Ala Asn Pro Glu Arg Ala Val Arg
465 470 475 480

Val Asn Ala Glu Asp Phe Val Gln Gln Thr Asp Gly Lys Tyr Lys Ala
485 490 495

Gly Leu Thr Ile Thr Gly Glu Asp Ala Pro Asn Leu Lys Asn Ile Ala
500 505 510

Phe His Glu Glu Asp Asn Asn Met Asn Asn Ile Ile Leu Phe Val Gly
515 520 525

Thr Asp Ala Ala Asp Val Ile Tyr Leu Asp Asn Ile Lys Val Ile Gly
530 535 540

Thr Glu Val Glu Ile Pro Val Val His Asp Pro Lys Gly Glu Ala Val
545 550 555 560

Leu Pro Ser Val Phe Glu Asp Gly Thr Arg Gln Gly Trp Asp Trp Ala
565 570 575

Gly Glu Ser Gly Val Lys Thr Ala Leu Thr Ile Glu Glu Ala Asn Gly
580 585 590

Ser Asn Ala Leu Ser Trp Glu Phe Gly Tyr Pro Glu Val Lys Pro Ser
595 600 605

Asp Asn Trp Ala Thr Ala Pro Arg Leu Asp Phe Trp Lys Ser Asp Leu
610 615 620

Val Arg Gly Glu Asn Asp Tyr Val Ala Phe Asp Phe Tyr Leu Asp Pro
625 630 635 640

Val Arg Ala Thr Glu Gly Ala Met Asn Ile Asn Leu Val Phe Gln Pro
645 650 655

Pro Thr Asn Gly Tyr Trp Val Gln Ala Pro Lys Thr Tyr Thr Ile Asn
660 665 670

Phe Asp Glu Leu Glu Glu Ala Asn Gln Val Asn Gly Leu Tyr His Tyr
675 680 685

Glu Val Lys Ile Asn Val Arg Asp Ile Thr Asn Ile Gln Asp Asp Thr
690 695 700

Leu Leu Arg Asn Met Met Ile Ile Phe Ala Asp Val Glu Ser Asp Phe

705

710

715

720

Ala Gly Arg Val Phe Val Asp Asn Val Arg Phe Glu Gly Ala Ala Thr
725 730 735

Thr Glu Pro Val Glu Pro Glu Pro Val Asp Pro Gly Glu Glu Thr Pro
740 745 750

Pro Val Asp Glu Lys Glu Ala Lys Lys Glu Gln Lys Glu Ala Glu Lys
755 760 765

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770 775 780

Lys Lys Ala Val Lys Asn Glu Ala Lys Lys Lys
785 790 795

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<212> DNA

<213> *Bacillus* sp. KSM-S237

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gaaataaaag tagaagacaa aggacataag aaaattgcat tagtttaat tatagaaaac 180

gccttttat aattatTTTat acctagaacg aaaatactgt ttccaaAGCG gtttactata	240
aaaccttata ttccggctct ttttAAAac agggggtaaa aattcactct agtattctaa	300
tttcaacatg ctataataaa tttgtaaagac gcaatATGca tctttttt tacgatata	360
gtaagcggTT aaccttgc tatatGCCga tttAGGAagg ggggtAGATT gagtcaagta	420
gtaataata agataactta taagttgtt agaAGCAGGA gagcatCTGG gttactcaca	480
agttttttt aaactttaac gaaAGCactt tcggtaatgc ttatGAATT agctatttga	540
ttcaattact ttaaaaatAT ttaggaggta AT ATG ATG TTA AGA AAG AAA ACA	593
Met Met Leu Arg Lys Lys Thr	
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aag cag ttg att tct tcc att ctt att tta gtt tta ctt cta tct tta	641
Lys Gin Leu Ile Ser Ser Ile Leu Ile Leu Val Leu Leu Ser Leu	
-20	
-15	
-10	
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Phe Pro Ala Ala Leu Ala Ala Glu Gly Asn Thr Arg Glu Asp Asn Phe	
-5	
-1	
1	
5	
10	
aaa cat tta tta ggt aat gac aat gtt aaa cgc cct tct gag gct ggc	737
Lys His Leu Leu Gly Asn Asp Asn Val Lys Arg Pro Ser Glu Ala Gly	
15	
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25	
gca tta caa tta caa gaa gtc gat gga caa atg aca tta gta gat caa	785
Ala Leu Gin Leu Gin Glu Val Asp Gly Gin Met Thr Leu Val Asp Gin	
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cat gga gaa aaa att caa tta cgt gga atg agt aca cac gga tta cag	833
His Gly Glu Lys Ile Gin Leu Arg Gly Met Ser Thr His Gly Leu Gin	
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tgg ttt cct gag atc ttg aat gat aac gca tac aaa gct ctt tct aac	881
Trp Phe Pro Glu Ile Leu Asn Asp Asn Ala Tyr Lys Ala Leu Ser Asn	
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gat tgg gat tcc aat atg att cgt ctt gct atg tat gta ggt gaa aat	929
Asp Trp Asp Ser Asn Met Ile Arg Leu Ala Met Tyr Val Gly Glu Asn	
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ggg tac gct aca aac cct gag tta atc aaa caa aga gtg att gat gga	977
Gly Tyr Ala Thr Asn Pro Glu Leu Ile Lys Gin Arg Val Ile Asp Gly	
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100	
105	

att gag tta gcg att gaa aat gac atg tat gtt att gtt gac tgg cat Ile Glu Leu Ala Ile Glu Asn Asp Met Tyr Val Ile Val Asp Trp His 110 115 120	1025
gtt cat gcg cca ggt gat cct aga gat cct gtt tat gca ggt gct aaa Val His Ala Pro Gly Asp Pro Arg Asp Pro Val Tyr Ala Gly Ala Lys 125 130 135	1073
gat ttc ttt aga gaa att gca gct tta tac cct aat aat cca cac att Asp Phe Phe Arg Glu Ile Ala Ala Leu Tyr Pro Asn Asn Pro His Ile 140 145 150	1121
att tat gag tta gcg aat gag ccg agt agt aat aat aat ggt gga gca Ile Tyr Glu Leu Ala Asn Glu Pro Ser Ser Asn Asn Asn Gly Gly Ala 155 160 165 170	1169
ggg att ccg aat aac gaa gaa ggt tgg aaa gcg gta aaa gaa tat gct Gly Ile Pro Asn Asn Glu Glu Gly Trp Lys Ala Val Lys Glu Tyr Ala 175 180 185	1217
gat cca att gta gaa atg tta cgt aaa agc ggt aat gca gat gac aac Asp Pro Ile Val Glu Met Leu Arg Lys Ser Gly Asn Ala Asp Asp Asn 190 195 200	1265
att atc att gtt ggt agt cca aac tgg agt cag cgt ccg gac tta gca Ile Ile Ile Val Gly Ser Pro Asn Trp Ser Gln Arg Pro Asp Leu Ala 205 210 215	1313
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tac act ggt tca cat gct gct tca act gaa agc tat ccg tct gaa act Tyr Thr Gly Ser His Ala Ala Ser Thr Glu Ser Tyr Pro Ser Glu Thr 235 240 245 250	1409
cct aac tct gaa aga gga aac gta atg agt aac act cgt tat gcg tta Pro Asn Ser Glu Arg Gly Asn Val Met Ser Asn Thr Arg Tyr Ala Leu 255 260 265	1457
gaa aac gga gta gcg gta ttt gca aca gag tgg gga acg agt caa gct Glu Asn Gly Val Ala Val Phe Ala Thr Glu Trp Gly Thr Ser Gln Ala 270 275 280	1505
agt gga gac ggt ggt cct tac ttt gat gaa gca gat gta tgg att gaa Ser Gly Asp Gly Gly Pro Tyr Phe Asp Glu Ala Asp Val Trp Ile Glu 285 290 295	1553
ttt tta aat gaa aac aac att agc tgg gct aac tgg tct tta acg aat	1601

Phe Leu Asn Glu Asn Asn Ile Ser Trp Ala Asn Trp Ser Leu Thr Asn			
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aaa aat gaa gta tct ggt gca ttt aca cca ttc gag tta ggt aag tct			1649
Lys Asn Glu Val Ser Gly Ala Phe Thr Pro Phe Glu Leu Gly Lys Ser			
315	320	325	330
aac gca acc aat ctt gac cca ggt cca gat cat gtg tgg gca cca gaa			1697
Asn Ala Thr Asn Leu Asp Pro Gly Pro Asp His Val Trp Ala Pro Glu			
335	340	345	
gaa tta agt ctt tct gga gaa tat gta cgt gct cgt att aaa ggt gtg			1745
Glu Leu Ser Leu Ser Gly Glu Tyr Val Arg Ala Arg Ile Lys Gly Val			
350	355	360	
aac tat gag cca atc gac cgt aca aaa tac acg aaa gta ctt tgg gac			1793
Asn Tyr Glu Pro Ile Asp Arg Thr Lys Tyr Thr Lys Val Leu Trp Asp			
365	370	375	
ttt aat gat gga acg aag caa gga ttt gga gtg aat tcg gat tct cca			1841
Phe Asn Asp Gly Thr Lys Gln Gly Phe Gly Val Asn Ser Asp Ser Pro			
380	385	390	
aat aaa gaa ctt att gca gtt gat aat gaa aac aac act ttg aaa gtt			1889
Asn Lys Glu Leu Ile Ala Val Asp Asn Glu Asn Asn Thr Leu Lys Val			
395	400	405	410
tcg gga tta gat gta agt aac gat gtt tca gat ggc aac ttc tgg gct			1937
Ser Gly Leu Asp Val Ser Asn Asp Val Ser Asp Gly Asn Phe Trp Ala			
415	420	425	
aat gct cgt ctt tct gcc aac ggt tgg gga aaa agt gtt gat att tta			1985
Asn Ala Arg Leu Ser Ala Asn Gly Trp Gly Lys Ser Val Asp Ile Leu			
430	435	440	
ggt gct gag aag ctt aca atg gat gtt att gtt gat gaa cca acg acg			2033
Gly Ala Glu Lys Leu Thr Met Asp Val Ile Val Asp Glu Pro Thr Thr			
445	450	455	
gta gct att gcg gcg att cca caa agt agt aaa agt gga tgg gca aat			2081
Val Ala Ile Ala Ala Ile Pro Gln Ser Ser Lys Ser Gly Trp Ala Asn			
460	465	470	
cca gag cgt gct gtt cga gtg aac gcg gaa gat ttt gtc cag caa acg			2129
Pro Glu Arg Ala Val Arg Val Asn Ala Glu Asp Phe Val Gln Gln Thr			
475	480	485	490
gac ggt aag tat aaa gct gga tta aca att aca gga gaa gat gct cct			2177
Asp Gly Lys Tyr Lys Ala Gly Leu Thr Ile Thr Gly Glu Asp Ala Pro			

495	500	505	
aac cta aaa aat atc gct ttt cat gaa gaa gat aac aat atg aac aac Asn Leu Lys Asn Ile Ala Phe His Glu Glu Asp Asn Asn Met Asn Asn 510	515	520	2225
atc att ctg ttc gtg gga act gat gca gct gac gtt att tac tta gat Ile Ile Leu Phe Val Gly Thr Asp Ala Ala Asp Val Ile Tyr Leu Asp 525	530	535	2273
aac att aaa gta att gga aca gaa gtt gaa att cca gtt gtt cat gat Asn Ile Lys Val Ile Gly Thr Glu Val Glu Ile Pro Val Val His Asp 540	545	550	2321
cca aaa gga gaa gct gtt ctt cct tct gtt ttt gaa gac ggt aca cgt Pro Lys Gly Glu Ala Val Leu Pro Ser Val Phe Glu Asp Gly Thr Arg 555	560	565	2369
caa ggt tgg gac tgg gct gga gag tct ggt gtg aaa aca gct tta aca Gln Gly Trp Asp Trp Ala Gly Glu Ser Gly Val Lys Thr Ala Leu Thr 575	580	585	2417
att gaa gaa gca aac ggt tct aac gcg tta tca tgg gaa ttt gga tat Ile Glu Glu Ala Asn Gly Ser Asn Ala Leu Ser Trp Glu Phe Gly Tyr 590	595	600	2465
cca gaa gta aaa cct agt gat aac tgg gca aca gct cca cgt tta gat Pro Glu Val Lys Pro Ser Asp Asn Trp Ala Thr Ala Pro Arg Leu Asp 605	610	615	2513
ttc tgg aaa tct gac ttg gtt cgc ggt gag aat gat tat gta gct ttt Phe Trp Lys Ser Asp Leu Val Arg Gly Glu Asn Asp Tyr Val Ala Phe 620	625	630	2561
gat ttc tat cta gat cca gtt cgt gca aca gaa ggc gca atg aat atc Asp Phe Tyr Leu Asp Pro Val Arg Ala Thr Glu Gly Ala Met Asn Ile 635	640	645	2609
aat tta gta ttc cag cca cct act aac ggg tat tgg gta caa gca cca Asn Leu Val Phe Gln Pro Pro Thr Asn Gly Tyr Trp Val Gln Ala Pro 655	660	665	2657
aaa acg tat acg att aac ttt gat gaa tta gag gaa gcg aat caa gta Lys Thr Tyr Thr Ile Asn Phe Asp Glu Leu Glu Ala Asn Gln Val 670	675	680	2705
aat ggt tta tat cac tat gaa gtg aaa att aac gta aga gat att aca Asn Gly Leu Tyr His Tyr Glu Val Lys Ile Asn Val Arg Asp Ile Thr 685	690	695	2753

aac att caa gat gac acg tta cta cgt aac atg atg atc att ttt gca Asn Ile Gln Asp Asp Thr Leu Leu Arg Asn Met Met Ile Ile Phe Ala 700 705 710	2801
gat gta gaa agt gac ttt gca ggg aga gtc ttt gta gat aat gtt cgt Asp Val Glu Ser Asp Phe Ala Gly Arg Val Phe Val Asp Asn Val Arg 715 720 725 730	2849
ttt gag ggg gct gct act act gag ccg gtt gaa cca gag cca gtt gat Phe Glu Gly Ala Ala Thr Thr Glu Pro Val Glu Pro Glu Pro Val Asp 735 740 745	2897
cct ggc gaa gag acg cca cct gtc gat gag aag gaa gcg aaa aaa gaa Pro Gly Glu Glu Thr Pro Pro Val Asp Glu Lys Glu Ala Lys Lys Glu 750 755 760	2945
caa aaa gaa gca gag aaa gaa gag aaa gaa gca gta aaa gaa gaa aag Gln Lys Glu Ala Glu Lys Glu Glu Lys Glu Ala Val Lys Glu Glu Lys 765 770 775	2993
aaa gaa gct aaa gaa gaa aag aaa gca gtc aaa aat gag gct aag aaa Lys Glu Ala Lys Glu Glu Lys Lys Ala Val Lys Asn Glu Ala Lys Lys 780 785 790	3041
aaa taatcttata aactagttat agggttatct aaaggctctga tgttagatctt Lys 795	3094
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Leu Arg Gly Met Ser Thr His Gly Leu Gln Trp Phe Pro Glu Ile Leu
50 55 60

Asn Asp Asn Ala Tyr Lys Ala Leu Ala Asn Asp Trp Glu Ser Asn Met
65 70 75 80

Ile Arg Leu Ala Met Tyr Val Gly Glu Asn Gly Tyr Ala Ser Asn Pro
85 90 95

Glu Leu Ile Lys Ser Arg Val Ile Lys Gly Ile Asp Leu Ala Ile Glu
100 105 110

Asn Asp Met Tyr Val Ile Val Asp Trp His Val His Ala Pro Gly Asp
115 120 125

Pro Arg Asp Pro Val Tyr Ala Gly Ala Glu Asp Phe Phe Arg Asp Ile
130 135 140

Ala Ala Leu Tyr Pro Asn Asn Pro His Ile Ile Tyr Glu Leu Ala Asn
145 150 155 160

Glu Pro Ser Ser Asn Asn Asn Gly Gly Ala Gly Ile Pro Asn Asn Glu
165 170 175

Glu Gly Trp Asn Ala Val Lys Glu Tyr Ala Asp Pro Ile Val Glu Met
180 185 190

Leu Arg Asp Ser Gly Asn Ala Asp Asp Asn Ile Ile Ile Val Gly Ser
195 200 205

Pro Asn Trp Ser Gln Arg Pro Asp Leu Ala Ala Asp Asn Pro Ile Asp
210 215 220

Asp His His Thr Met Tyr Thr Val His Phe Tyr Thr Gly Ser His Ala
225 230 235 240

Ala Ser Thr Glu Ser Tyr Pro Pro Glu Thr Pro Asn Ser Glu Arg Gly
245 250 255

Asn Val Met Ser Asn Thr Arg Tyr Ala Leu Glu Asn Gly Val Ala Val
260 265 270

Phe Ala Thr Glu Trp Gly Thr Ser Gln Ala Asn Gly Asp Gly Gly Pro
275 280 285

Tyr Phe Asp Glu Ala Asp Val Trp Ile Glu Phe Leu Asn Glu Asn Asn
290 295 300

Ile Ser Trp Ala Asn Trp Ser Leu Thr Asn Lys Asn Glu Val Ser Gly
305 310 315 320

Ala Phe Thr Pro Phe Glu Leu Gly Lys Ser Asn Ala Thr Ser Leu Asp
325 330 335

Pro Gly Pro Asp Gln Val Trp Val Pro Glu Glu Leu Ser Leu Ser Gly
340 345 350

Glu Tyr Val Arg Ala Arg Ile Lys Gly Val Asn Tyr Glu Pro Ile Asp
355 360 365

Arg Thr Lys Tyr Thr Lys Val Leu Trp Asp Phe Asn Asp Gly Thr Lys
370 375 380

Gln Gly Phe Gly Val Asn Gly Asp Ser Pro Val Glu Asp Val Val Ile
385 390 395 400

Glu Asn Glu Ala Gly Ala Leu Lys Leu Ser Gly Leu Asp Ala Ser Asn
405 410 415

Asp Val Ser Glu Gly Asn Tyr Trp Ala Asn Ala Arg Leu Ser Ala Asp
420 425 430

Gly Trp Gly Lys Ser Val Asp Ile Leu Gly Ala Glu Lys Leu Thr Met
435 440 445

Asp Val Ile Val Asp Glu Pro Thr Thr Val Ser Ile Ala Ala Ile Pro
450 455 460

Gln Gly Pro Ser Ala Asn Trp Val Asn Pro Asn Arg Ala Ile Lys Val
465 470 475 480

Glu Pro Thr Asn Phe Val Pro Leu Gly Asp Lys Phe Lys Ala Glu Leu
485 490 495

Thr Ile Thr Ser Ala Asp Ser Pro Ser Leu Glu Ala Ile Ala Met His
500 505 510

Ala Glu Asn Asn Asn Ile Asn Asn Ile Ile Leu Phe Val Gly Thr Glu
515 520 525

Gly Ala Asp Val Ile Tyr Leu Asp Asn Ile Lys Val Ile Gly Thr Glu
530 535 540

Val Glu Ile Pro Val Val His Asp Pro Lys Gly Glu Ala Val Leu Pro
545 550 555 560

Ser Val Phe Glu Asp Gly Thr Arg Gln Gly Trp Asp Trp Ala Gly Glu
565 570 575

Ser Gly Val Lys Thr Ala Leu Thr Ile Glu Glu Ala Asn Gly Ser Asn
580 585 590

Ala Leu Ser Trp Glu Phe Gly Tyr Pro Glu Val Lys Pro Ser Asp Asn
595 600 605

Trp Ala Thr Ala Pro Arg Leu Asp Phe Trp Lys Ser Asp Leu Val Arg
610 615 620

Gly Glu Asn Asp Tyr Val Thr Phe Asp Phe Tyr Leu Asp Pro Val Arg

625

630

635

640

Ala Thr Glu Gly Ala Met Asn Ile Asn Leu Val Phe Gln Pro Pro Thr
645 650 655

Asn Gly Tyr Trp Val Gln Ala Pro Lys Thr Tyr Thr Ile Asn Phe Asp
660 665 670

Glu Leu Glu Glu Ala Asn Gln Val Asn Gly Leu Tyr His Tyr Glu Val
675 680 685

Lys Ile Asn Val Arg Asp Ile Thr Asn Ile Gln Asp Asp Thr Leu Leu
690 695 700

Arg Asn Met Met Ile Ile Phe Ala Asp Val Glu Ser Asp Phe Ala Gly
705 710 715 720

Arg Val Phe Val Asp Asn Val Arg Phe Glu Gly Ala Ala Thr Thr Glu
725 730 735

Pro Val Glu Pro Glu Pro Val Asp Pro Gly Glu Glu Thr Pro Pro Val
740 745 750

Asp Glu Lys Glu Ala Lys Lys Glu Gln Lys Glu Ala Glu Lys Glu Glu
755 760 765

Lys Glu Ala Val Lys Glu Glu Lys Lys Glu Ala Lys Glu Glu Lys Lys
770 775 780

Ala Ile Lys Asn Glu Ala Thr Lys Lys
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<210> 7

<211> 3332

<212> DNA

<213> *Bacillus* sp. KSM-64

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<223>

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<221> mat_peptide
<222> (697).. (3075)
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cctgatttta ttttttgaa ttttttgag aactaaagat tgaaaatagaa gttagaagaca 180
acggacataa gaaaattgta ttagtttaa ttatagaaaa cgctttcta taattattta 240
tacctagaac gaaaatactg tttcgaaagc gtttactat aaaaccttattt attccggctc 300
ttttttaaa cagggggtaa aaattcactc tagtattcta atttcaacat gctataataa 360
attttaaga cgcaatatac atctttttt tatgatattt gtaagcggtt aaccttgc 420
tatatgccga ttttaggaagg gggtagattt agtcaagtag tcataattta gataacttat 480
aagtgttga gaagcaggag agaatctggg ttactcacaa gtttttaaaa acattatcga 540
aagcacttcc ggttatgctt atgaatttttag ctatttgcattt caattactttt aataatttt 600
ggaggtaat atg atg tta aga aag aaa aca aag cag ttg att tct tcc att 651
Met Met Leu Arg Lys Lys Thr Lys Gln Leu Ile Ser Ser Ile
-25 -20

ctt att tta gtt tta ctt cta tct tta ttt ccg aca gct ctt gca gca 699
Leu Ile Leu Val Leu Leu Ser Leu Phe Pro Thr Ala Leu Ala Ala
-15 -10 -5 -1 1

gaa gga aac act cgt gaa gac aat ttt aaa cat tta tta ggt aat gac 747
Glu Gly Asn Thr Arg Glu Asp Asn Phe Lys His Leu Leu Gly Asn Asp
5 10 15

aat gtt aaa cgc cct tct gag gct ggc gca tta caa tta caa gaa gtc 795
Asn Val Lys Arg Pro Ser Glu Ala Gly Ala Leu Gln Leu Gln Glu Val

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20	25	30	
gat gga caa atg aca tta gta gat caa cat gga gaa aaa att caa tta Asp Gly Gln Met Thr Leu Val Asp Gln His Gly Glu Lys Ile Gln Leu 35 40 45			843
cgt gga atg agt aca cac gga tta caa tgg ttt cct gag atc ttg aat Arg Gly Met Ser Thr His Gly Leu Gln Trp Phe Pro Glu Ile Leu Asn 50 55 60 65			891
gat aac gca tac aaa gct ctt gct aac gat tgg gaa tca aat atg att Asp Asn Ala Tyr Lys Ala Leu Ala Asn Asp Trp Glu Ser Asn Met Ile 70 75 80			939
cgt cta gct atg tat gtc ggt gaa aat ggc tat gct tca aat cca gag Arg Leu Ala Met Tyr Val Gly Glu Asn Gly Tyr Ala Ser Asn Pro Glu 85 90 95			987
tta att aaa agc aga gtc att aaa gga ata gat ctt gct att gaa aat Leu Ile Lys Ser Arg Val Ile Lys Gly Ile Asp Leu Ala Ile Glu Asn 100 105 110			1035
gac atg tat gtc atc gtt gat tgg cat gta cat gca cct ggt gat cct Asp Met Tyr Val Ile Val Asp Trp His Val His Ala Pro Gly Asp Pro 115 120 125			1083
aga gat ccc gtt tac gct gga gca gaa gat ttc ttt aga gat att gca Arg Asp Pro Val Tyr Ala Gly Ala Glu Asp Phe Phe Arg Asp Ile Ala 130 135 140 145			1131
gca tta tat cct aac aat cca cac att att tat gag tta gcg aat gag Ala Leu Tyr Pro Asn Asn Pro His Ile Ile Tyr Glu Leu Ala Asn Glu 150 155 160			1179
cca agt agt aac aat aat ggt gga gct ggg att cca aat aat gaa gaa Pro Ser Ser Asn Asn Asn Gly Gly Ala Gly Ile Pro Asn Asn Glu Glu 165 170 175			1227
ggt tgg aat gcg gta aaa gaa tac gct gat cca att gta gaa atg tta Gly Trp Asn Ala Val Lys Glu Tyr Ala Asp Pro Ile Val Glu Met Leu 180 185 190			1275
cgt gat agc ggg aac gca gat gac aat att atc att gtg ggt agt cca Arg Asp Ser Gly Asn Ala Asp Asp Asn Ile Ile Val Gly Ser Pro 195 200 205			1323
aac tgg agt cag cgt cct gac tta gca gct gat aat cca att gat gat Asn Trp Ser Gln Arg Pro Asp Leu Ala Ala Asp Asn Pro Ile Asp Asp 210 215 220 225			1371

cac cat aca atg tat act gtt cac ttc tac act ggt tca cat gct gct			1419
His His Thr Met Tyr Thr Val His Phe Tyr Thr Gly Ser His Ala Ala			
230	235	240	
tca act gaa agc tat ccg cct gaa act cct aac tct gaa aga gga aac			1467
Ser Thr Glu Ser Tyr Pro Pro Glu Thr Pro Asn Ser Glu Arg Gly Asn			
245	250	255	
gta atg agt aac act cgt tat gcg tta gaa aac gga gta gca gta ttt			1515
Val Met Ser Asn Thr Arg Tyr Ala Leu Glu Asn Gly Val Ala Val Phe			
260	265	270	
gca aca gag tgg gga act agc caa gca aat gga gat ggt ggt cct tac			1563
Ala Thr Glu Trp Gly Thr Ser Gln Ala Asn Gly Asp Gly Pro Tyr			
275	280	285	
ttt gat gaa gca gat gta tgg att gag ttt tta aat gaa aac aac att			1611
Phe Asp Glu Ala Asp Val Trp Ile Glu Phe Leu Asn Glu Asn Asn Ile			
290	295	300	305
agc tgg gct aac tgg tct tta acg aat aaa aat gaa gta tct ggt gca			1659
Ser Trp Ala Asn Trp Ser Leu Thr Asn Lys Asn Glu Val Ser Gly Ala			
310	315	320	
ttt aca cca ttc gag tta ggt aag tct aac gca aca agt ctt gac cca			1707
Phe Thr Pro Phe Glu Leu Gly Lys Ser Asn Ala Thr Ser Leu Asp Pro			
325	330	335	
ggg cca gac caa gta tgg gta cca gaa gag tta agt ctt tct gga gaa			1755
Gly Pro Asp Gln Val Trp Val Pro Glu Glu Leu Ser Leu Ser Gly Glu			
340	345	350	
tat gta cgt gct cgt att aaa ggt gtg aac tat gag cca atc gac cgt			1803
Tyr Val Arg Ala Arg Ile Lys Gly Val Asn Tyr Glu Pro Ile Asp Arg			
355	360	365	
aca aaa tac acg aaa gta ctt tgg gac ttt aat gat gga acg aag caa			1851
Thr Lys Tyr Thr Lys Val Leu Trp Asp Phe Asn Asp Gly Thr Lys Gln			
370	375	380	385
gga ttt gga gtg aat gga gat tct cca gtt gaa gat gta gtt att gag			1899
Gly Phe Gly Val Asn Gly Asp Ser Pro Val Glu Asp Val Val Ile Glu			
390	395	400	
aat gaa gcg ggc gct tta aaa ctt tca gga tta gat gca agt aat gat			1947
Asn Glu Ala Gly Ala Leu Lys Leu Ser Gly Leu Asp Ala Ser Asn Asp			
405	410	415	

gtt tct gaa ggt aat tac tgg gct aat gct cgt ctt tct gcc gac ggt Val Ser Glu Gly Asn Tyr Trp Ala Asn Ala Arg Leu Ser Ala Asp Gly 420 425 430	1995
tgg gga aaa agt gtt gat att tta ggt gct gaa aaa ctt act atg gat Trp Gly Lys Ser Val Asp Ile Leu Gly Ala Glu Lys Leu Thr Met Asp 435 440 445	2043
gtg att gtt gat gag ccg acc acg gta tca att gct gca att cca caa Val Ile Val Asp Glu Pro Thr Thr Val Ser Ile Ala Ala Ile Pro Gln 450 455 460 465	2091
ggg cca tca gcc aat tgg gtt aat cca aat cgt gca att aag gtt gag Gly Pro Ser Ala Asn Trp Val Asn Pro Asn Arg Ala Ile Lys Val Glu 470 475 480	2139
cca act aat ttc gta ccg tta gga gat aag ttt aaa gcg gaa tta act Pro Thr Asn Phe Val Pro Leu Gly Asp Lys Phe Lys Ala Glu Leu Thr 485 490 495	2187
ata act tca gct gac tct cca tcg tta gaa gct att gcg atg cat gct Ile Thr Ser Ala Asp Ser Pro Ser Leu Glu Ala Ile Ala Met His Ala 500 505 510	2235
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gct gat gtt atc tat tta gat aac att aaa gta att gga aca gaa gtt Ala Asp Val Ile Tyr Leu Asp Asn Ile Lys Val Ile Gly Thr Glu Val 530 535 540 545	2331
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gtt ttt gaa gac ggt aca cgt caa ggt tgg gac tgg gct gga gag tct Val Phe Glu Asp Gly Thr Arg Gln Gly Trp Asp Trp Ala Gly Glu Ser 565 570 575	2427
ggt gtg aaa aca gct tta aca att gaa gaa gca aac ggt tct aac gcg Gly Val Lys Thr Ala Leu Thr Ile Glu Glu Ala Asn Gly Ser Asn Ala 580 585 590	2475
tta tca tgg gaa ttt gga tac cca gaa gta aaa cct agt gat aac tgg Leu Ser Trp Glu Phe Gly Tyr Pro Glu Val Lys Pro Ser Asp Asn Trp 595 600 605	2523
gca aca gct cca cgt tta gat ttc tgg aaa tct gac ttg gtt cgc ggt	2571

Ala Thr Ala Pro Arg Leu Asp Phe Trp Lys Ser Asp Leu Val Arg Gly			
610	615	620	625
gaa aat gat tat gta act ttt gat ttc tat cta gat cca gtt cgt gca			2619
Glu Asn Asp Tyr Val Thr Phe Asp Phe Tyr Leu Asp Pro Val Arg Ala			
630	635	640	
aca gaa ggc gca atg aat atc aat tta gta ttc cag cca cct act aac			2667
Thr Glu Gly Ala Met Asn Ile Asn Leu Val Phe Gln Pro Pro Thr Asn			
645	650	655	
ggg tat tgg gta caa gca cca aaa acg tat acg att aac ttt gat gaa			2715
Gly Tyr Trp Val Gln Ala Pro Lys Thr Tyr Thr Ile Asn Phe Asp Glu			
660	665	670	
tta gag gaa gcg aat caa gta aat ggt tta tat cac tat gaa gtg aaa			2763
Leu Glu Glu Ala Asn Gln Val Asn Gly Leu Tyr His Tyr Glu Val Lys			
675	680	685	
att aac gta aga gat att aca aac att caa gat gac acg tta cta cgt			2811
Ile Asn Val Arg Asp Ile Thr Asn Ile Gln Asp Asp Thr Leu Leu Arg			
690	695	700	705
aac atg atg atc att ttt gca gat gta gaa agt gac ttt gca ggg aga			2859
Asn Met Met Ile Ile Phe Ala Asp Val Glu Ser Asp Phe Ala Gly Arg			
710	715	720	
gtc ttt gta gat aat gtt cgt ttt gag ggg gct gct act act gag ccg			2907
Val Phe Val Asp Asn Val Arg Phe Glu Gly Ala Ala Thr Thr Glu Pro			
725	730	735	
gtt gaa cca gag cca gtt gat cct ggc gaa gag acg ccg cct gtc gat			2955
Val Glu Pro Glu Pro Val Asp Pro Gly Glu Glu Thr Pro Pro Val Asp			
740	745	750	
gag aag gaa gcg aaa aaa gaa caa aaa gaa gca gag aaa gaa gag aaa			3003
Glu Lys Glu Ala Lys Lys Glu Gln Lys Glu Ala Glu Lys Glu Glu Lys			
755	760	765	
gaa gca gta aaa gaa gaa aag aaa gaa gct aaa gaa gaa aag aaa gca			3051
Glu Ala Val Lys Glu Glu Lys Lys Glu Ala Lys Glu Glu Lys Lys Ala			
770	775	780	785
atc aaa aat gag gct acg aaa aaa taatctaata aactagttat agggttatct			3105
Ile Lys Asn Glu Ala Thr Lys Lys			
790			
aaaggctctga tgcagatctt ttagataacc ttttttgca taactggaca tagaatggtt			3165

attaaagaaa gcaagggttt tatacgatat taaaaaggta gcgatttaa attgaaacct 3225
ttaataatgt ctgtgtatag aatgtatgtaa taatttaaga ggggaaacg aagtgaaaac 3285
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<210> 8
<211> 20
<212> DNA
<213> artificial sequence

<220>
<223> Oligonucleotide as PCR primer designed from nucleotide sequence o
f sigA in *Bacillus subtilis*

<400> 8
atggctgata aacaaaccca 20

<210> 9
<211> 20
<212> DNA
<213> artificial sequence

<220>
<223> Oligonucleotide as PCR primer designed from nucleotide sequence o
f sigA in *Bacillus subtilis*

<400> 9
caccacaatg ttcatggca 20

<210> 10
<211> 21
<212> DNA
<213> artificial sequence

<220>
<223> Oligonucleotide as PCR primer designed from nucleotide sequence o
f the upstream region of sigH in *Bacillus subtilis*

<400> 10
acagccttcc ttccctcattc t 21

<210> 11
<211> 42
<212> DNA

<213> artificial sequence

<220>

<223> Oligonucleotide as PCR primer; its 3'-portion designed from nucleotide sequence of the upstream region of sigH in *Bacillus subtilis* and its 5'-portion designed from nucleotide sequence of sigA in *Bacillus subtilis*

<400> 11

cgtgggttg tttatcagcc attccgatcc ccccgccgca cg 42

<210> 12

<211> 21

<212> DNA

<213> artificial sequence

<220>

<223> Oligonucleotide as PCR primer designed from nucleotide sequence of the upstream region of sigF in *Bacillus subtilis*

<400> 12

gctgatagaa cgtgacacgg g 21

<210> 13

<211> 42

<212> DNA

<213> artificial sequence

<220>

<223> Oligonucleotide as PCR primer; its 3'-portion designed from nucleotide sequence of the upstream region of sigF in *Bacillus subtilis* and its 5'-portion designed from nucleotide sequence of sigA in *Bacillus subtilis*

<400> 13

cgtgggttg tttatcagcc atgctcattc ctccctgata tg 42

<210> 14

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<212> DNA

<213> artificial sequence

<220>

<223> Oligonucleotide as PCR primer designed from nucleotide sequence of plasmid pC194

<400> 14
caactaaagc acccattag 19

<210> 15
<211> 44
<212> DNA
<213> artificial sequence

<220>
<223> Oligonucleotide as PCR primer; its 3'-portion designed from nucleotide sequence of plasmid pC194 and its 5'-portion designed from nucleotide sequence of sigA in *Bacillus subtilis*

<400> 15
catttgcaaa tgaacattgt ggtgcttctt caactaacgg ggca 44

<210> 16
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<212> DNA
<213> artificial sequence

<220>
<223> Oligonucleotide as PCR primer designed from nucleotide sequence of sigA in *Bacillus subtilis*; the sequence containing a nucleotide substitution for destroying the initiation codon of sigA

<400> 16
atagctgata aacaaacccca 20

<210> 17
<211> 42
<212> DNA
<213> artificial sequence

<220>
<223> Oligonucleotide as PCR primer; its 3'-portion designed from nucleotide sequence of the upstream region of sigF in *Bacillus subtilis* and its 5'-portion designed from nucleotide sequence of sigA in *Bacillus subtilis*; the sequence containing a nucleotide substitution for destroying the initiation codon of sigA

<400> 17
cgtgggtttg tttatcagct atgctcattc ctcccttgata tg 42

<210> 18

<211> 1795
<212> DNA
<213> *Bacillus* sp. KSM-K38

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<223>

<220>
<221> sig_peptide
<222> (212)..(274)
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<221> mat_peptide
<222> (275)..(1714)
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<400> 18

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aaatgacatc atataaacaa atttgtctac caatcactat ttaaagctgt ttatgtatata	180
tgtaagcggt atcattaaaa ggaggtatTTT g ATG AGA AGA TGG Gta Gta Gca Met Arg Arg Trp Val Val Ala -20 -15	232
atg ttg gca gtg tta ttt tta ttt cct tcg gta gta gtt gca gat gga Met Leu Ala Val Leu Phe Leu Phe Pro Ser Val Val Val Ala Asp Gly -10 -5 -1 1	280
ttg aac ggt acg atg atg cag tat tat gag tgg cat ttg gaa aac gac Leu Asn Gly Thr Met Met Gln Tyr Tyr Glu Trp His Leu Glu Asn Asp 5 10 15	328
ggc cag cat tgg aat cgg ttg cac gat gat gcc gca gct ttg agt gat Gly Gln His Trp Asn Arg Leu His Asp Asp Ala Ala Leu Ser Asp 20 25 30	376
gct ggt att aca gct att tgg att ccg cca gcc tac aaa ggt aat agt Ala Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Tyr Lys Gly Asn Ser 35 40 45 50	424
cag gcg gat gtt ggg tac ggt gca tac gat ctt tat gat tta gga gag Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu Gly Glu	472

55	60	65	
ttc aat caa aag ggt act gtt cga acg aaa tac gga act aag gca cag Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ala Gln 70	75	80	520
ctt gaa cga gct att ggg tcc ctt aaa tct aat gat atc aat gta tac Leu Glu Arg Ala Ile Gly Ser Leu Lys Ser Asn Asp Ile Asn Val Tyr 85	90	95	568
gga gat gtc gtg atg aat cat aaa atg gga gct gat ttt acg gag gca Gly Asp Val Val Met Asn His Lys Met Gly Ala Asp Phe Thr Glu Ala 100	105	110	616
gtg caa gct gtt caa gta aat cca acg aat cgt tgg cag gat att tca Val Gln Ala Val Gln Val Asn Pro Thr Asn Arg Trp Gln Asp Ile Ser 115	120	125	130
ggt gcc tac acg att gat gcg tgg acg ggt ttc gac ttt tca ggg cgt Gly Ala Tyr Thr Ile Asp Ala Trp Thr Gly Phe Asp Phe Ser Gly Arg 135	140	145	712
aac aac gcc tat tca gat ttt aag tgg aga tgg ttc cat ttt aat ggt Asn Asn Ala Tyr Ser Asp Phe Lys Trp Arg Trp Phe His Phe Asn Gly 150	155	160	760
gtt gac tgg gat cag cgc tat caa gaa aat cat att ttc cgc ttt gca Val Asp Trp Asp Gln Arg Tyr Gln Glu Asn His Ile Phe Arg Phe Ala 165	170	175	808
aat acg aac tgg aac tgg cga gtg gat gaa gag aac ggt aat tat gat Asn Thr Asn Trp Asn Trp Arg Val Asp Glu Glu Asn Gly Asn Tyr Asp 180	185	190	856
tac ctg tta gga tcg aat atc gac ttt agt cat cca gaa gta caa gat Tyr Leu Leu Gly Ser Asn Ile Asp Phe Ser His Pro Glu Val Gln Asp 195	200	205	904
gag ttg aag gat tgg ggt agc tgg ttt acc gat gag tta gat ttg gat Glu Leu Lys Asp Trp Gly Ser Trp Phe Thr Asp Glu Leu Asp Leu Asp 215	220	225	952
ggt tat cgt tta gat gct att aaa cat att cca ttc tgg tat aca tct Gly Tyr Arg Leu Asp Ala Ile Lys His Ile Pro Phe Trp Tyr Thr Ser 230	235	240	1000
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gta ggg gaa tat tgg aag gat gac gta ggt gct ctc gaa ttt tat tta			1096
Val Gly Glu Tyr Trp Lys Asp Asp Val Gly Ala Leu Glu Phe Tyr Leu			
260	265	270	
gat gaa atg aat tgg gag atg tct cta ttc gat gtt cca ctt aat tat			1144
Asp Glu Met Asn Trp Glu Met Ser Leu Phe Asp Val Pro Leu Asn Tyr			
275	280	285	290
aat ttt tac cgg gct tca caa caa ggt gga agc tat gat atg cgt aat			1192
Asn Phe Tyr Arg Ala Ser Gln Gln Gly Gly Ser Tyr Asp Met Arg Asn			
295	300	305	
att tta cga gga tct tta gta gaa gcg cat ccg atg cat gca gtt acg			1240
Ile Leu Arg Gly Ser Leu Val Glu Ala His Pro Met His Ala Val Thr			
310	315	320	
ttt gtt gat aat cat gat act cag cca ggg gag tca tta gag tca tgg			1288
Phe Val Asp Asn His Asp Thr Gln Pro Gly Glu Ser Leu Glu Ser Trp			
325	330	335	
gtt gct gat tgg ttt aag cca ctt gct tat gcg aca att ttg acg cgt			1336
Val Ala Asp Trp Phe Lys Pro Leu Ala Tyr Ala Thr Ile Leu Thr Arg			
340	345	350	
gaa ggt ggt tat cca aat gta ttt tac ggt gat tac tat ggg att cct			1384
Glu Gly Gly Tyr Pro Asn Val Phe Tyr Gly Asp Tyr Tyr Gly Ile Pro			
355	360	365	370
aac gat aac att tca gct aaa aaa gat atg att gat gag ctg ctt gat			1432
Asn Asp Asn Ile Ser Ala Lys Lys Asp Met Ile Asp Glu Leu Leu Asp			
375	380	385	
gca cgt caa aat tac gca tat ggc acg cag cat gac tat ttt gat cat			1480
Ala Arg Gln Asn Tyr Ala Tyr Gly Thr Gln His Asp Tyr Phe Asp His			
390	395	400	
tgg gat gtt gta gga tgg act agg gaa gga tct tcc tcc aga cct aat			1528
Trp Asp Val Val Gly Trp Thr Arg Glu Gly Ser Ser Arg Pro Asn			
405	410	415	
tca ggc ctt gcg act att atg tcg aat gga cct ggt ggt tcc aag tgg			1576
Ser Gly Leu Ala Thr Ile Met Ser Asn Gly Pro Gly Gly Ser Lys Trp			
420	425	430	
atg tat gta gga cgt cag aat gca gga caa aca tgg aca gat tta act			1624
Met Tyr Val Gly Arg Gln Asn Ala Gly Gln Thr Trp Thr Asp Leu Thr			
435	440	445	450

ggt aat aac gga gcg tcc gtt aca att aat ggc gat gga tgg ggc gaa 1672
Gly Asn Asn Gly Ala Ser Val Thr Ile Asn Gly Asp Gly Trp Gly Glu
455 460 465

ttc ttt acg aat gga gga tct gta tcc gtg tac gtg aac caa taacaaaaa 1723
Phe Phe Thr Asn Gly Gly Ser Val Ser Val Tyr Val Asn Gln
470 475 480

gccttgagaa gggattcctc ccttaactcaa ggctttcttt atgtcgctta gctttacgct 1783
tctacgactt tg 1795

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<211> 480
<212> PRT
<213> *Bacillus* sp. KSM-K38

<400> 19

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Asn Asp Gly Gln His Trp Asn Arg Leu His Asp Asp Ala Ala Ala Leu
20 25 30

Ser Asp Ala Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Tyr Lys Gly
35 40 45

Asn Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu
50 55 60

Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
65 70 75 80

Ala Gln Leu Glu Arg Ala Ile Gly Ser Leu Lys Ser Asn Asp Ile Asn
85 90 95

Val Tyr Gly Asp Val Val Met Asn His Lys Met Gly Ala Asp Phe Thr
100 105 110

Glu Ala Val Gln Ala Val Gln Val Asn Pro Thr Asn Arg Trp Gln Asp

115 120 125

Ile Ser Gly Ala Tyr Thr Ile Asp Ala Trp Thr Gly Phe Asp Phe Ser
130 135 140

Gly Arg Asn Asn Ala Tyr Ser Asp Phe Lys Trp Arg Trp Phe His Phe
145 150 155 160

Asn Gly Val Asp Trp Asp Gln Arg Tyr Gln Glu Asn His Ile Phe Arg
165 170 175

Phe Ala Asn Thr Asn Trp Asn Trp Arg Val Asp Glu Glu Asn Gly Asn
180 185 190

Tyr Asp Tyr Leu Leu Gly Ser Asn Ile Asp Phe Ser His Pro Glu Val
195 200 205

Gln Asp Glu Leu Lys Asp Trp Gly Ser Trp Phe Thr Asp Glu Leu Asp
210 215 220

Leu Asp Gly Tyr Arg Leu Asp Ala Ile Lys His Ile Pro Phe Trp Tyr
225 230 235 240

Thr Ser Asp Trp Val Arg His Gln Arg Asn Glu Ala Asp Gln Asp Leu
245 250 255

Phe Val Val Gly Glu Tyr Trp Lys Asp Asp Val Gly Ala Leu Glu Phe
260 265 270

Tyr Leu Asp Glu Met Asn Trp Glu Met Ser Leu Phe Asp Val Pro Leu
275 280 285

Asn Tyr Asn Phe Tyr Arg Ala Ser Gln Gln Gly Ser Tyr Asp Met
290 295 300

Arg Asn Ile Leu Arg Gly Ser Leu Val Glu Ala His Pro Met His Ala
305 310 315 320

Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Glu Ser Leu Glu
325 330 335

Ser Trp Val Ala Asp Trp Phe Lys Pro Leu Ala Tyr Ala Thr Ile Leu
340 345 350

Thr Arg Glu Gly Gly Tyr Pro Asn Val Phe Tyr Gly Asp Tyr Tyr Gly
355 360 365

Ile Pro Asn Asp Asn Ile Ser Ala Lys Lys Asp Met Ile Asp Glu Leu
370 375 380

Leu Asp Ala Arg Gln Asn Tyr Ala Tyr Gly Thr Gln His Asp Tyr Phe
385 390 395 400

Asp His Trp Asp Val Val Gly Trp Thr Arg Glu Gly Ser Ser Arg
405 410 415

Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asn Gly Pro Gly Gly Ser
420 425 430

Lys Trp Met Tyr Val Gly Arg Gln Asn Ala Gly Gln Thr Trp Thr Asp
435 440 445

Leu Thr Gly Asn Asn Gly Ala Ser Val Thr Ile Asn Gly Asp Gly Trp
450 455 460

Gly Glu Phe Phe Thr Asn Gly Gly Ser Val Ser Val Tyr Val Asn Gln
465 470 475 480

<210> 20

<211> 1441

<212> DNA

<213> *Bacillus clausii* KSM-K16

<220>

<221> CDS

<222> (164)..(1303)

<223>

<400> 20

tggtagcttt ccccaacttga aaccgtttta atcaaaaaac aaagtggaa aattctgtta 60

acttaatgtt aataattgtt tcccaatagg caaatcttc taactttgat acgtttaaac 120

taccagcttg gacgagttgg gataaaagtg aggagggAAC cga atg aag aaa ccg 175
Met Lys Lys Pro
1

ttg ggg aaa att gtc gca agc acc gca cta ctc att tct gtt gct ttt 223
Leu Gly Lys Ile Val Ala Ser Thr Ala Leu Leu Ile Ser Val Ala Phe
5 10 15 20

agt tca tcg atc gca tcg gct gct gag gaa gca aaa gaa aaa tat tta 271
Ser Ser Ser Ile Ala Ser Ala Ala Glu Glu Ala Lys Glu Lys Tyr Leu
25 30 35

att ggc ttt aat gag cag gaa gca gtt agt gag ttt gta gag caa ata 319
Ile Gly Phe Asn Glu Gln Glu Ala Val Ser Glu Phe Val Glu Gln Ile
40 45 50

gag gca aat gac gat gtc gcg att ctc tct gag gaa gag gaa gtc gaa 367
Glu Ala Asn Asp Asp Val Ala Ile Leu Ser Glu Glu Glu Val Glu
55 60 65

att gaa ttg ctt cat gag ttt gaa acg att cct gtt tta tct gtt gag 415
Ile Glu Leu Leu His Glu Phe Glu Thr Ile Pro Val Leu Ser Val Glu
70 75 80

tta agt cca gaa gat gtg gac gcg ctt gag ctc gat cca acg att tcg 463
Leu Ser Pro Glu Asp Val Asp Ala Leu Glu Leu Asp Pro Thr Ile Ser
85 90 95 100

tat att gaa gag gat gca gaa gta acg aca atg gcg caa tca gtg cca 511
Tyr Ile Glu Glu Asp Ala Glu Val Thr Thr Met Ala Gln Ser Val Pro
105 110 115

tgg gga att agc cgt gta caa gcc cca gct gcc cat aac cgt gga ttg 559
Trp Gly Ile Ser Arg Val Gln Ala Pro Ala Ala His Asn Arg Gly Leu
120 125 130

aca ggt tct ggt gta aaa gtt gct gtc ctc gat acg ggt att tcc acc 607
Thr Gly Ser Gly Val Lys Val Ala Val Leu Asp Thr Gly Ile Ser Thr
135 140 145

cat cca gac tta aat att cgc ggt ggt gct acg ttt gtg cca gga gaa 655

His Pro Asp Leu Asn Ile Arg Gly Gly Ala Ser Phe Val Pro Gly Glu			
150	155	160	
cca tcc actcaa gat gga aat gga cat ggc acg cat gtg gca ggg acg			703
Pro Ser Thr Gln Asp Gly Asn Gly His Gly Thr His Val Ala Gly Thr			
165	170	175	180
att gct gct tta aac aat tcg att ggc gtt ctg ggc gta gca ccg acg			751
Ile Ala Ala Leu Asn Asn Ser Ile Gly Val Leu Gly Val Ala Pro Ser			
185	190	195	
gcg gaa cta tac gct gta aaa gta tta ggc gcg acg ggt tca ggt tcg			799
Ala Glu Leu Tyr Ala Val Lys Val Leu Gly Ala Ser Gly Ser Gly Ser			
200	205	210	
gtc agc tcg att gcc caa gga ttg gaa tgg gca ggg aac aat ggc atg			847
Val Ser Ser Ile Ala Gln Gly Leu Glu Trp Ala Gly Asn Asn Gly Met			
215	220	225	
cac gtt gcg aat ttg agt tta gga agc ccg tcg ccg agt gca aca ctt			895
His Val Ala Asn Leu Ser Leu Gly Ser Pro Ser Pro Ser Ala Thr Leu			
230	235	240	
gag caa gct gtt aat agc gct act tct aga ggc gtt ctt gtc gta gca			943
Glu Gln Ala Val Asn Ser Ala Thr Ser Arg Gly Val Leu Val Val Ala			
245	250	255	260
gca tct ggt aat tca ggt gca ggc tca atc agc tat ccg gcc cgt tat			991
Ala Ser Gly Asn Ser Gly Ala Gly Ser Ile Ser Tyr Pro Ala Arg Tyr			
265	270	275	
gcg aac gca atg gca gtc gga gcg act gac caa aac aac aac cgc gct			1039
Ala Asn Ala Met Ala Val Gly Ala Thr Asp Gln Asn Asn Asn Arg Ala			
280	285	290	
agc ttt tca cag tat gga gct ggg ctt gac att gtc gcg cca ggt gtc			1087
Ser Phe Ser Gln Tyr Gly Ala Gly Leu Asp Ile Val Ala Pro Gly Val			
295	300	305	
aat gtg cag agc aca tac cca ggt tca aca tat gcc agc tta aac ggt			1135
Asn Val Gln Ser Thr Tyr Pro Gly Ser Thr Tyr Ala Ser Leu Asn Gly			
310	315	320	
aca tcg atg gct act cct cat gtt gca ggt gta gca gcc ctt gtt aaa			1183
Thr Ser Met Ala Thr Pro His Val Ala Gly Val Ala Ala Leu Val Lys			
325	330	335	340
caa aag aat cca tct tgg tcc aat gta caa atc cgc aat cat cta aag			1231
Gln Lys Asn Pro Ser Trp Ser Asn Val Gln Ile Arg Asn His Leu Lys			

345

350

355

aat acg gca acg ggt tta gga aac acg aac ttg tat gga agc ggg ctt 1279
 Asn Thr Ala Thr Gly Leu Gly Asn Thr Asn Leu Tyr Gly Ser Gly Leu
 360 365 370

gtc aat gca gaa gcg gca aca cgc taatcaataa taataacgct gtgtgctta 1333
 Val Asn Ala Glu Ala Ala Thr Arg
 375 380

agcacacagc gtttttagt gtgtatgaat cgaaaaagag aaatagatcg ctgattcaa 1393

aaagcgagcg taaagggcta ttgaagctct ttacgcttgc aggatttg 1441

<210> 21

<211> 380

<212> PRT

<213> *Bacillus clausii* KSM-K16

<400> 21

Met Lys Lys Pro Leu Gly Lys Ile Val Ala Ser Thr Ala Leu Leu Ile
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Ser Val Ala Phe Ser Ser Ser Ile Ala Ser Ala Ala Glu Glu Ala Lys
 20 25 30

Glu Lys Tyr Leu Ile Gly Phe Asn Glu Gln Glu Ala Val Ser Glu Phe
 35 40 45

Val Glu Gln Ile Glu Ala Asn Asp Asp Val Ala Ile Leu Ser Glu Glu
 50 55 60

Glu Glu Val Glu Ile Glu Leu Leu His Glu Phe Glu Thr Ile Pro Val
 65 70 75 80

Leu Ser Val Glu Leu Ser Pro Glu Asp Val Asp Ala Leu Glu Leu Asp
 85 90 95

Pro Thr Ile Ser Tyr Ile Glu Glu Asp Ala Glu Val Thr Thr Met Ala
 100 105 110

Gln Ser Val Pro Trp Gly Ile Ser Arg Val Gln Ala Pro Ala Ala His
115 120 125

Asn Arg Gly Leu Thr Gly Ser Gly Val Ala Val Leu Asp Thr
130 135 140

Gly Ile Ser Thr His Pro Asp Leu Asn Ile Arg Gly Gly Ala Ser Phe
145 150 155 160

Val Pro Gly Glu Pro Ser Thr Gln Asp Gly Asn Gly His Gly Thr His
165 170 175

Val Ala Gly Thr Ile Ala Ala Leu Asn Asn Ser Ile Gly Val Leu Gly
180 185 190

Val Ala Pro Ser Ala Glu Leu Tyr Ala Val Lys Val Leu Gly Ala Ser
195 200 205

Gly Ser Gly Ser Val Ser Ser Ile Ala Gln Gly Leu Glu Trp Ala Gly
210 215 220

Asn Asn Gly Met His Val Ala Asn Leu Ser Leu Gly Ser Pro Ser Pro
225 230 235 240

Ser Ala Thr Leu Glu Gln Ala Val Asn Ser Ala Thr Ser Arg Gly Val
245 250 255

Leu Val Val Ala Ala Ser Gly Asn Ser Gly Ala Gly Ser Ile Ser Tyr
260 265 270

Pro Ala Arg Tyr Ala Asn Ala Met Ala Val Gly Ala Thr Asp Gln Asn
275 280 285

Asn Asn Arg Ala Ser Phe Ser Gln Tyr Gly Ala Gly Leu Asp Ile Val
290 295 300

Ala Pro Gly Val Asn Val Gln Ser Thr Tyr Pro Gly Ser Thr Tyr Ala
305 310 315 320

Ser Leu Asn Gly Thr Ser Met Ala Thr Pro His Val Ala Gly Val Ala
325 330 335

Ala Leu Val Lys Gln Lys Asn Pro Ser Trp Ser Asn Val Gln Ile Arg
340 345 350

Asn His Leu Lys Asn Thr Ala Thr Gly Leu Gly Asn Thr Asn Leu Tyr
355 360 365

Gly Ser Gly Leu Val Asn Ala Glu Ala Ala Thr Arg
370 375 380

<210> 22

<211> 46

<212> DNA

<213> Artificial

<220>

<223> Oligonucleotide as PCR primer; its 3'-portion designed from nucleotide sequence of the alkaline protease gene in *Bacillus clausii* KSM-K16 and its 5'-portion designed from nucleotide sequence of the upstream region of the alkaline cellulase gene in *Bacillus* sp. KSM-S237

<400> 22

actttaaaaa tatttaggag gtaatatgaa gaaaccgttg gggaaaa 46

<210> 23

<211> 32

<212> DNA

<213> Artificial

<220>

<223> Oligonucleotide as PCR primer designed from nucleotide sequence of the downstream region of the alkaline protease gene in *Bacillus clausii* KSM-K16 with a insertion of the BgIII restriction site at the 5'-end

<400> 23

gggagatctt cagcgatcta tttcttttt tc 32

<210> 24
<211> 25
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide as PCR primer designed from nucleotide sequence of the upstream region of the alkaline cellulase gene in *Bacillus* sp. KSM-S237 with a insertion of the BamHI restriction site at the 5'-end

<400> 24
cccgatcca acaggcttat attta 25

<210> 25
<211> 46
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide as PCR primer; its 3'-portion designed from nucleotide sequence of the upstream region of the alkaline cellulase gene in *Bacillus* sp. KSM-S237 and its 5'-portion designed from nucleotide sequence of the alkaline protease gene in *Bacillus* clausii KSM-K16

<400> 25
tttccccaaac ggtttcttca tattacctcc taaatattt taaagt 46

<210> 26
<211> 30
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide as PCR primer; its 3'-portion designed from nucleotide sequence of the alkaline amylase gene in *Bacillus* sp. KSM-K38 and its 5'-portion designed from nucleotide sequence of the alkaline cellulase gene in *Bacillus* sp. KSM-S237

<400> 26
gctcttgac cagatggatt gaacggtagc 30

<210> 27
<211> 30
<212> DNA
<213> Artificial

<220>

<223> Oligonucleotide as PCR primer designed from nucleotide sequence of the downstream region of the alkaline amylase gene in *Bacillus* sp. KSM-K38 with a insertion of the XbaI restriction site at the 5'-end

<400> 27

ttggtctaga ccccaagctt caaagtcgta

30

<210> 28
<211> 29
<212> DNA
<213> Artificial

<220>

<223> Oligonucleotide as PCR primer: its 3'-portion designed from nucleotide sequence of the alkaline cellulase gene in *Bacillus* sp. KSM-S237 and its 5'-portion designed from nucleotide sequence of the alkaline amylase gene in *Bacillus* sp. KSM-K38

<400> 28

ttcaatccat ctgctgcaag agctgccgg

29